CLAIMS

1. Apparatus for analysing a polynucleotide sequence, comprising a support and attached to a surface thereof an array of the whole or a chosen part of a complete set of oligonucleotides of chosen lengths, the different oligonucleotides occupying separate cells of the array and being capable of taking part in hybridisation reactions.

2. Apparatus for studying differences between polynucleotide sequences, comprising a support and attached to a surface thereof an array of the whole or a chosen part of a complete set of oligonucleotides of chosen lengths comprising the polynucleotide sequences, the diferent oligonucleotides occupying separate cells of the array and being capable of taking part in hybridisation reactions.

3. Apparatus as claimed in claim 2, wherein the array comprises one or more pairs of oligonucleotides of chosen lengths.

4. Apparatus as claimed in claim 3, wherein the array comprises one or more pairs of oligonucleotides of chosen lengths representing normal and mutant versions of a point mutation to be studied.

5. Apparatus as claimed in any one of claims 1 or 2, wherein the chosen length is from 8 to 20 nucleotides.

6. Apparatus as claimed in any one of claims 1 or 2, wherein the surface of the support to which the oligonucleotides are attached is of glass.

7. Apparatus as claimed in any one of claims 1 or 2, wherein each oligonucleotide is bound to the support through a covalent link.

8. A method of analysing a polynucleotide sequence, by the use of a support to the surface of which is attached an array of the whole or a chosen part of a complete set of oligonucleotides of chosen lengths, the different oligonucleotides occupying separate cells of the array, which method comprises labelling the polynucleotide sequence or fragments thereof to form labelled material,

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applying the labelled material under hybridisation conditions to the array, and observing the location of the label on the surface associated with particular members of the set of oligonucleotides.

9. A method according to claim 8, applied to the study of differences between polynucleotide sequences, wherein the array is of the whole or a chosen part of the complete set of oligonucleotides of chosen lengths comprising the polynucleotide sequences.

10. The method as claimed in claim 9, wherein the array comprises one or more pairs of oligonucleotides of chosen lengths.

11. The method as claimed in claim 10, wherein the array comprises one or more pairs of oligonucleotides of chosen lengths representing normal and mutant versions of a point mutation being studied.

12. The method according to any one of claims 8 to 11, wherein the polynucleotide sequence is randomly degraded to form a mixture of oligomers of a chosen length, the mixture being thereafter labelled to form the labelled material.

13. The method as claimed in claim 12, wherein the oligomers are labelled with $^{32}P$.

14. The method as claimed in any one of claims 8 to 11, wherein the chosen length is from 8 to 20 nucleotides.

15. The method as claimed in claim 8, where the set of oligonucleotides is attached to the surface as an array of parallel stripes, and at least two polynucleotide sequences are analysed simultaneously by applying the labelled material to the array in the form of separate stripes orthogonal to the oligonucleotide stripes.

16. The method as claimed in claim 8, wherein hybridisation is effected in the presence of tetramethylammoniumchloride at a concentration of 1M to 5M.